

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 31, 2005, 18:02:30 ; Search time 148.167 Seconds  
(without alignments)  
54.366 Million cell updates/sec

Title: US-10-083-768-12  
Perfect score: 85  
Sequence: 1 CADGPTLEWISFC 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_02.\*

1: uniprot\_spot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 53    | 62.4        | 297    | 2     | Q7UQE4 rhodopirell |
| 2          | 50.5  | 59.4        | 387    | 2     | Q98A97 rhizobium l |
| 3          | 50.5  | 59.4        | 389    | 2     | Q8KJF9 rhizobium l |
| 4          | 48    | 56.5        | 1123   | 2     | Q7QC63 anopheles g |
| 5          | 47.5  | 55.9        | 283    | 2     | Q82CW2 streptomyce |
| 6          | 46    | 54.1        | 319    | 2     | Q9RKM5 streptomyce |
| 7          | 46    | 54.1        | 347    | 2     | Q7PPP6 anopheles g |
| 8          | 45    | 52.9        | 108    | 2     | Q7RUAS neuropsora  |
| 9          | 45    | 52.9        | 173    | 2     | Q8C4M6 mus musculu |
| 10         | 45    | 52.9        | 209    | 2     | Q6N1X5 rhodopsenu  |
| 11         | 45    | 52.9        | 209    | 2     | CAE29718 rhodopsu  |
| 12         | 45    | 52.9        | 309    | 2     | Q8XZM5 raistonia s |
| 13         | 45    | 52.9        | 443    | 2     | Q9P858 phaeosphaer |
| 14         | 44    | 51.8        | 173    | 2     | Q6QHD2 gallid herp |
| 15         | 44    | 51.8        | 173    | 2     | AAE48543 gallid he |
| 16         | 44    | 51.8        | 178    | 2     | Q6PL14 gallid herp |
| 17         | 44    | 51.8        | 178    | 2     | AAE09767 gallid he |
| 18         | 44    | 51.8        | 209    | 2     | Q9L059 streptomyce |
| 19         | 44    | 51.8        | 292    | 2     | Q67642 gallid herp |
| 20         | 44    | 51.8        | 298    | 2     | Q86653 gallid herp |
| 21         | 44    | 51.8        | 974    | 1     | PHS2 SOLTU         |
| 22         | 44    | 51.8        | 997    | 2     | Q6BI26 debaryomyce |
| 23         | 44    | 51.8        | 1008   | 2     | Q8AY57 fundulus he |
| 24         | 44    | 51.8        | 1011   | 2     | Q6VYM7 oncorhynch  |
| 25         | 44    | 51.8        | 1011   | 2     | AAQ82787           |
| 26         | 44    | 51.8        | 1022   | 1     | AT1A TORCA         |
| 27         | 44    | 51.8        | 1023   | 1     | ALAI HUMAN         |
| 28         | 44    | 51.8        | 1025   | 2     | Q7ZYK8 xenopus lae |
| 29         | 44    | 51.8        | 1028   | 1     | ALAI4 RAT          |
| 30         | 43.5  | 51.2        | 405    | 2     | Q9KIE9 streptomyce |
| 31         | 43.5  | 51.2        | 934    | 2     | Q9NEX6 caenorhabdi |

32 43 50.6 127 2 Q9N0Z5  
33 43 50.6 171 2 Q8HYW6  
34 43 50.6 176 2 Q866A9  
35 43 50.6 245 2 Q9M060  
36 43 50.6 407 2 Q6NMU4  
37 43 50.6 407 2 Q9VK55  
38 43 50.6 407 2 AA515697  
39 43 50.6 469 2 Q37839  
40 43 50.6 490 2 Q04270  
41 43 50.6 509 2 Q88IG9  
42 43 50.6 960 2 Q80U28  
43 43 50.6 962 2 Q91Y19  
44 43 50.6 1000 2 Q7Z419  
45 43 50.6 1009 2 Q98SL3

## ALIGNMENTS

RESULT 1  
Q7UQE4 PRELIMINARY; PRT; 297 AA.  
AC Q7UQE4, 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocusNames=RB6375;  
OS Rhodopirellula baltica.  
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;  
OC Planctomycetaceae; Pirellula.  
OX NCBI\_TaxID=117;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1;  
RX MEDLINE=22735913; PubMed=12835416;  
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,  
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,  
RA Schlesner H., Amann R., Reinhardt R.;  
RT "Complete genome sequence of the marine planctomycete Pirellula sp.  
RT strain 1.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).  
RR EMBL; BX294144; CAD74759.1;  
DR InterPro; IPR00194; ATPase\_a/bcentre.  
DR InterPro; IPR003169; GVF.  
DR PROSITE; PS00152; ATPASE\_ALPHA\_BETA; UNKNOWN\_1.  
DR PROSITE; PS50823; GVF; 1.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 297 AA; 31805 MW; 475F670F02C78E9B CRC64;

Query Match 62.4%; Score 53; DB 2; Length 297;  
Best Local Similarity 72.7%; Pred. No. 1.1;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ADGPTLEWIS 12  
| | | | | : : : : :  
Db 175 ADGPTLEWIS 185

RESULT 2  
Q98A97 PRELIMINARY; PRT; 387 AA.  
AC Q98A97, 01-OCT-2001 (TrEMBLrel. 18, Created)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Mlr6096 protein.  
GN OrderedLocusNames=mlr6096;  
OS Rhizobium loti (Mesorhizobium loti).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Phyllobacteriaceae; Mesorhizobium.  
OX NCBI\_TaxID=381;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=WAFF030099;  
RX MEDLINE=21082936; PubMed=11214974;  
RA Kaneko T., Nakamura Y., Sato S., Asanizu E., Kato T., Sasamoto S.,  
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,  
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,  
RA Takeuchi C., Yamada M., Tabata S.;  
RP "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
RT *Mesorhizobium loti* (supplement).";  
RT Mesorhizobium loti (supplement).";  
RN DNA Res. 7:381-406(2000).  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WAFF030099;  
RX MEDLINE=21082930; PubMed=11214968;  
RA Kaneko T., Nakamura Y., Sato S., Asanizu E., Kato T., Sasamoto S.,  
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,  
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,  
RA Takeuchi C., Yamada M., Tabata S.;  
RP "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
RT *Mesorhizobium loti*.";  
RT Mesorhizobium loti.";  
RN DNA Res. 7:331-338(2000).  
DR EMBL; AP0031008; BABS2440.1; --  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR003673; CA1B\_BAIF.  
DR Pfam; PF02515; COA\_transf\_3; 1.  
DR Complete proteome.  
SQ SEQUENCE 387 AA; 42226 MW; 64643EBEC8F25518 CRC64;

|                       |        |              |       |             |
|-----------------------|--------|--------------|-------|-------------|
| Query Match           | 59.4%; | Score 50.5;  | DB 2; | Length 387; |
| Best Local Similarity | 42.9%; | Pred. No. 4; |       |             |
| Matches               | 9:     | Conservative | 3:    | Mismatches  |
|                       |        |              | 2:    | Indels      |
|                       |        |              | 7:    | Gaps        |

Qy 1 CADGPTL-----REWISFC 14  
 |||| : ||||: ||  
 Db 237 CADGKEVIFS VONDREWVNEC 25

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RESULT 3
Q8KJF9
ID Q8KJF9 PRELIMINARY; PRT; 389 AA.
AC Q8KJF9;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE PUTATIVE RACEMASE/DEHYDRATASE PROTEIN.
GN Name=ml181;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI TaxID=381;

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|    |  |
|----|--|
| RP | SEQUENCE FROM N.A.   |
| RC | STRAIN=R7A;  |
| RX | MEDLINE=21999272; Pubmed=12003951;                                   |
| RA | Sullivan J.T., Trebatowski J.R., Cruickshank R.W., Guzy J.,          |
| RA | Brown S.D., Elliot R.M., Fleetwood D.J., McCallum N.G., Rossbach U., |
| RA | Stuart G.S., Weaver J.E., Webby R.J., de Bruijn F.J., Ronsch C.W.;   |
| RT | "Comparative sequence analysis of the symbiosis island of            |
| RT | Mesorhizobium loti strain R7A.";                                     |
| RL | J. Bacteriol. 184:3086-3095 (2002).                                  |
| DR | EWBL: AL672113; CAD31586.1; -.                                       |
| DR | GO: GO:0008152; P:metabolism; IEA.                                   |
| DR | Interpro: IPR003673; CAIB:BAIF.                                      |
| DR | Pfam: PF02515; COA:trans_3; 1.                                       |
| SO | SEQUENCE 389 AA: 42703 MW; 6678D2C96A7E5204 CRC64;                   |

Query Match 59.4%; Score 50.5; DB 2; Length 389;  
Best Local Similarity 42.9%; Pred. No. 4;  
Matches 9; Conservative 3; Mismatches 2; Indels 7; Gaps 1

OV 1 CADGPTL-----REWISFC 14

243 CADGKEVIFSVQNDREWWFC 263

```

RESULT 4
7QC63
ID Q7QC63 PRELIMINARY; PRT; 1123 AA.
AC AC
AT 07QC63;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE AgCP1221.
GN Name=agCG531078; ORFNames=ENSANGG00000018866;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Anopheles
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

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DR EMBL; AAB0100859; EAA08177.1; --  
DR GO:0005524: F:ATP binding; IEA.

DR GO:0008898; F:homocysteine S-methyltransferase activity; IEA.  
 NP GO:0004672; F:protein kinase activity; IEA.

DR GO:00016740; F:transferase activity; IEA.  
DP GO:00005468; P:protein amino acid phosphorylation; IEA.

[illegible]

DR PF0069; pkinaase; 1.  
PF0074; 8-methyl-  
DR PF0074; 8-methyl-  
DR PF0074; 8-methyl-

DR PFam; PF02574; S-methyl trans; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.

DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
SQ SEQUENCE 1123 AA; 120006 MW; D3CC001D8D4882AF CRC64;

| Query Match | Score 48; | DB 2; | Length 1123; |
|-------------|-----------|-------|--------------|
| 56.5%       | Score 48; | DB 2; | Length 1123; |

Best Local Similarity 75.0%; Pred. NO. 34;  
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0

|    |     |              |    |
|----|-----|--------------|----|
| Qy | 2   | ADGPTLREWISF | 13 |
|    |     |              |    |
|    |     |              |    |
|    |     |              |    |
|    |     | :            | :  |
|    |     |              |    |
| Db | 969 | ADHPTVREWISF | 98 |

## RESULT 5

|        |  |              |
|--------|--|--------------|
| Q82CW2 | PRELIMINARY;   | PRT; 203 AA. |
| ID     | Q82CW2   |              |
| AC     | Q82CW2;  |              |
| DT     | 01-JUN-2003 (TrEMBLrel. 24, Created)                         |              |
| DT     | 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)            |              |
| DT     | 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)          |              |
| DE     | Purative ICB-family transcriptional regulator.               |              |
| GN     | OrderedLocNames=SAV5226;                                     |              |
| OS     | Streptomyces avermitilis.                                    |              |
| OC     | Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; |              |
| OC     | Streptomycinae; Streptomycetaceae; Streptomyces.             |              |
| OX     | NCBI TaxID=133903;   |              |

RN [1]  
PD SEQUENCE FROM N. A.

RC STRAIN=MA-4680;  
PV MEDV.TIN=21477A03; DithMed-11572948.

RA MEDLINE=2147403; PubMed=11572310;  
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,  
RA Chinese M. Melchiorri V. Horikawa H. Nakazawa H. Osone T.

RA SHINJOSE M., IZAKAWASHI I., NOIRIKAWA H., NAKAZAWA H., OCHINOBI  
RA KIKUCHI H., SHIBA T., SAKAKI Y., HATTORI M.;  
RA "Industrial and Commercial Development of  
Strentomvices

RT avermitilis: deducing the ability of producing secondary

RT metabolites.";  
Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).  
RL

RN [2]

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Db      258 DGPELREWL 267
|||||:::
RESULT 7
Q7PFP6 PRELIMINARY; PRT; 347 AA.
ID AC Q7PFP6;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE ENSANGP0000020769 (Fragment).
GN Name=ENSANGG00000018280;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/Genbank/DDbj databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DDbj whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAA01008944; EAA10075.2; -.
DR GO; GO:0008898; F:homocysteine S-methyltransferase activity; IEA.
DR InterPro; IPR003726; S_methyl_trans.
DR Pfam; PF02574; S-methyl_trans; 1.
FT NON TER 1
SQ SEQUENCE 347 AA; 38585 MW; 66FF58A100CDA4F CRC64;

Query Match 54.1%; Score 46; DB 2; Length 347;
Best Local Similarity 61.5%; Pred. No. 21;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps

Qy 1 CADGPTLEWISF 13
|:::|||||
Db 201 CDEYPTVRFWISF 213

RESULT 8
Q7RUAS PRELIMINARY; PRT; 108 AA.
ID AC Q7RUAS;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Hypothetical protein B24B19.30.
GN Name=NCU03933.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=0874A;
RA Galsagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Selicrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysysselis M., Maucelli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metznerberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Flammann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbote D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RA "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).

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DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
GN RPA4277.
OS Rhodopseudomonas palustris.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodospseudomonas.
OX NCBI_TaxID=1076;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707;
RA Larimer F.W., Chain P., Hauser L., Lamerdin J., Malfatti S., Do L.,
RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,
RA Harrison F.H., Gibson J., Harwood C.S.;
RA "Complete genome sequence of the metabolically versatile
RT photosynthetic bacterium Rhodospseudomonas palustris.";
RL Nat. Biotechnol. 22:55-61(2004).
DR EMBL; BX572606; CAE29718.1; -.
KW Hypothetical protein.
SQ SEQUENCE 209 AA; 23238 MW; 6FE082A84DB040EE CRC64;

Query Match 52.9%; Score 45; DB 2; Length 209;
Best Local Similarity 50.0%; Pred. No. 19;
Matches 9; Conservative 2; Mismatches 1; Indels 6; Gaps 1;

QY 1 CADG-----PTLREWIS 12
   ||| ||| ||| |||
DB 98 CADTGYEAALPTIREWLS 115

RESULT 12
Q8XZN5 Q8XZN5 PRELIMINARY; PRT; 309 AA.
AC Q8XZN5;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE PROBABLE TRANSCRIPTION REGULATOR PROTEIN.
GN Name=RS04642; OrderedLocusNames=RS1360;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Sigulier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RA "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL645064; CAD15062.1; -.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000847; HTH_LysR.
DR InterPro; IPR005119; LysR_subst.
DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PROSITE; PS00931; HTH_LysR; 1.
KW Complete proteome.
SQ SEQUENCE 309 AA; 33774 MW; 733551741CE83182 CRC64;

Query Match 52.9%; Score 45; DB 2; Length 309;
Best Local Similarity 70.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 CADGPTLREW 10
   ||| ||| |||
DB 221 CTDCANVLEW 230

RESULT 13
Q9P858 Q9P858 PRELIMINARY; PRT; 443 AA.
AC Q9P858;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Phaeosphaeria nodorum (Septoria nodorum).
OG Plasmid plsal.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Phaeosphaeriaceae; Phaeosphaeria.
OX NCBI_TaxID=13684;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BS444;
RA Rawson J.M.;
RT "Transposable elements in the phytopathogenic fungus Stagonospora
RL nodorum.";
RL Thesis (2000), PhD thesis, University of Birmingham,UK.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BS444;
RA Rawson J.M., Cutler S.B., Caten C.E.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ277966; CAB91876.1; -.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 443 AA; 49466 MW; 367E0762EE839E68 CRC64;

Query Match 52.9%; Score 45; DB 2; Length 443;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CADGPTLREWIS 12
   ||: ||| ||| |||
DB 170 CSENGTLREWIT 181

RESULT 14
Q6QHD2 Q6QHD2 PRELIMINARY; PRT; 173 AA.
AC Q6QHD2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE P32 (Fragment).
OS Gallid herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Infectious laryngotracheitis-like viruses.
OX NCBI_TaxID=10386;
RN [1]
RP SEQUENCE FROM N.A.
RA Villarreal L.Y., Brandao P.E., Ferreira A.P., Doretto L.J.,
RA D'elboux A.N.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY541676; AAS48543.1; -.
DR InterPro; IPR007110; Ig-like.
FT NON_TER 1
FT NON_TER 173
SQ SEQUENCE 173 AA; 19130 MW; 5AE4A1956CEB9B13 CRC64;

Query Match 51.8%; Score 44; DB 2; Length 173;
Best Local Similarity 50.0%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 CADGPTLREWISFC 14
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Db      120 CLDMPPLRPWTTC 133

RESULT 15
AAS48543
ID AAS48543 PRELIMINARY; PRT; 173 AA.
AC AAS48543;
DT 10-MAR-2004 (TREMELrel. 27, Created)
DT 10-MAR-2004 (TREMELrel. 27, Last sequence update)
DT 10-MAR-2004 (TREMELrel. 27, Last annotation update)
DE F32 (Fragment).
OS Gallid herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Infectious laryngotracheitis-like viruses.
OX NCBI_TaxID=10386;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP01;
RA Villarreal L.Y., Brandao P.E., Ferreira A.P., Doretto L.J.,
RA D'elboux A.N.;
RT "Molecular epidemiology of an outbreak of infectious laryngotracheitis
RT in Brazilian poultry.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY541676; AAS48543.1; -.
FT NON_TER 1
FT NON_TER 173
SQ SEQUENCE 173 AA; 19130 MW; 5AE4A1956CEB9B13 CRC64;

Query Match 51.8%; Score 44; DB 2; Length 173;
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Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 CADGPTLRWISFC 14
Db      120 CLDMPPLRPWTTC 133

Search completed: January 31, 2005, 18:21:43
Job time : 151.167 secs

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